

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Coleman, Roger  
Bandman, Olga
- (ii) TITLE OF THE INVENTION: NOVEL HUMAN C5A-LIKE RECEPTOR
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Drive
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Herewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0198 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 415-855-0555
  - (B) TELEFAX: 415-845-4166
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 333 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: Consensus
  - (B) CLONE: 346374
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Thr	Asn	Ser	Ser	Phe	Phe	Cys	Pro	Val	Tyr	Lys	Asp	Leu	Glu	Pro
1				5					10					15	
Phe	Thr	Tyr	Phe	Phe	Tyr	Leu	Val	Phe	Leu	Val	Gly	Ile	Ile	Gly	Ser
			20					25					30		
Cys	Phe	Ala	Thr	Trp	Ala	Phe	Ile	Gln	Lys	Asn	Thr	Asn	His	Arg	Cys
	35					40					45				
Val	Ser	Ile	Tyr	Leu	Ile	Asn	Leu	Leu	Thr	Ala	Asp	Phe	Leu	Leu	Thr
	50				55						60				
Leu	Ala	Leu	Pro	Val	Lys	Ile	Val	Val	Asp	Leu	Gly	Val	Ala	Pro	Trp
65				70					75					80	
Lys	Leu	Lys	Ile	Phe	His	Cys	Gln	Val	Thr	Ala	Cys	Leu	Ile	Tyr	Ile
			85					90					95		
Asn	Met	Tyr	Leu	Ser	Ile	Ile	Phe	Leu	Ala	Phe	Val	Ser	Ile	Asp	Arg
			100					105					110		
Cys	Leu	Gln	Leu	Thr	His	Ser	Cys	Lys	Ile	Tyr	Arg	Ile	Gln	Glu	Pro
	115						120					125			
Gly	Phe	Ala	Lys	Met	Ile	Ser	Thr	Val	Val	Trp	Leu	Met	Val	Leu	Leu
	130				135						140				
Ile	Met	Val	Pro	Asn	Met	Met	Ile	Pro	Ile	Lys	Asp	Ile	Lys	Glu	Lys
145				150						155				160	
Ser	Asn	Val	Gly	Cys	Met	Glu	Phe	Lys	Lys	Glu	Phe	Gly	Arg	Asn	Trp
			165					170					175		
His	Leu	Leu	Thr	Asn	Phe	Ile	Cys	Val	Ala	Ile	Phe	Leu	Asn	Phe	Ser
	180						185						190		
Ala	Ile	Ile	Leu	Ile	Ser	Asn	Cys	Leu	Val	Ile	Arg	Gln	Leu	Tyr	Arg
	195						200				205				
Asn	Lys	Arg	Asn	Gln	Asn	Tyr	Pro	Asp	Val	Lys	Lys	Ala	Leu	Ile	Asn
	210				215					220					
Ile	Leu	Leu	Val	Thr	Thr	Gly	Tyr	Ile	Ile	Cys	Phe	Val	Pro	Tyr	His
225				230						235				240	
Ile	Val	Arg	Ile	Pro	Tyr	Thr	Leu	Ser	Gln	Thr	Glu	Val	Ile	Thr	Asp
			245					250					255		
Cys	Ser	Thr	Arg	Ile	Ser	Leu	Phe	Lys	Ala	Lys	Glu	Ala	Thr	Leu	Leu
		260					265						270		
Leu	Ala	Val	Ser	Asn	Leu	Cys	Phe	Asp	Pro	Ile	Leu	Tyr	Tyr	His	Leu
	275					280					285				
Ser	Lys	Ala	Phe	Arg	Ser	Lys	Val	Thr	Glu	Thr	Phe	Ala	Ser	Pro	Lys
	290					295					300				
Glu	Thr	Lys	Ala	Gln	Lys	Gln	Lys	Leu	Arg	Cys	Glu	Asn	Asn	Ala	
305				310						315					

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1257 base pairs

(B) ORGANISM: Homo sapiens

(C) STRANDEDNESS: single

(D) RESEARCH USE ONLY

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 346874

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGCTCATGC	TTTCTGGAAG	ACTTGCAGCA	AGGCTTGCTG	AGGCTCACAG	AAGATAGCCC	60
CAGTGTTTTG	GAGTGGTTTT	GAATGTGATT	CTGAGATCAG	ACTGACTGAG	CTGGGAATCCT	120
GGCTTTATAT	CTTACAGAGT	ACWCAAGCTT	GGAGTCTTAG	AAATTTTTC	TTTTCATTAA	180
GCAGTCATCC	TTACTTTCCC	TCAAGATGAC	AAACAGTTCC	TTCTTCTGCC	CAGTTTATAA	240
AGATCTGGAG	CCATTCAAGT	ATTTTCTTA	TTTAGTTTC	CTTGTGGAA	TTATTGGAAG	300
TTGTTTTCGA	ACCTGGGCTT	TTATACAGAA	GAATACGAAT	CACAGGTGTG	TGAGCATCTA	360

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CTTAATAAAT TTGCTTACAG CCGATTTCCT GTTACTCTTG GCATTACCAG TGAAAATTGT 430
TGTTGACTTG GGTGTGGCAC CTGGGAARCT GAAGATATTC CACTGCCAAG TAACAGCCTG 430
CCTCATCTAT ATCAATATGT ATTTATCAAT TATCTTCTTA GCATTGTGCA GCATTGACCG 540
CTGTCTTCAG CTGACACACA GCTGCAAGAT CTACCGAATA CAAGAACCOC GGTTTGCCAA 600
AATGATATCA ACCGTGTGTG GGCTAATGGT CTTCTTTATA ATGGTGCCAA ATATGATGAT 660
TCCCATCAAA GACATCAAGG AAAAGTCAAA TGTGGGTTGT ATGGAGTTTA AAAAGGAATT 720
TGGAAGAAAT TGGCATTTGC TGACAAAATTT CATATGTGTA GCAATATTTT TAAATTTCTC 780
AGCCATCATT TTAATATCCA ATTGCTTTGT AATTCGACAG CTCTACAGAA ACAAAGATAA 840
TGAAAATTAC CCAAAATGTGA AAAAGGCTCT CATCAACATA CTTTTAGTGA CCACGGGCTA 900
CATCAPATGC TTTGTTCCTT ACCACATTGT CCGAATCCCG TATACCCCTCA GCCAGACAGA 960
AGTCATAACT GATTGCTCAA CCAGGATTTC ACTCTTCAAA GCCAAAGAGG CTACACTGCT 1020
CCTGGCTGTG TCGAACCTGT GCTTTGATCC TATCTGTGAC TATCACCTCT CAAAAGCATT 1080
CCGCTCAAAG GTCACTGAGA CTTTTCGCTC ACCTAAAGAG ACCAAGGCTC AGAAAGAAAA 1140
ATTAAGATGT GAAAATAATG CATAAAAGAC AGGATTTTCT GTGCTACCAA TTCTGGCCTT 1200
ACTGGACCAT AAAGTTAATT ATAGCTTTGA AAGATAAAAA AAAAAAAAAA AAAAAAA 1257

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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 115257

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Asn Ser Phe Asn Tyr Thr Thr Pro Asp Tyr Gly His Tyr Asp Asp
1      5      10      15
Lys Asp Thr Leu Asp Leu Asn Thr Pro Val Asp Lys Thr Ser Asn Thr
20      25      30
Leu Arg Val Pro Asp Ile Leu Ala Leu Val Ile Phe Ala Val Val Phe
35      40      45
Leu Val Gly Val Leu Gly Asn Ala Leu Val Val Trp Val Thr Ala Phe
50      55      60
Glu Ala Lys Arg Thr Ile Asn Ala Ile Trp Phe Leu Asn Leu Ala Val
65      70      75      80
Ala Asp Phe Leu Ser Cys Leu Ala Leu Pro Ile Leu Phe Thr Ser Ile
85      90      95
Val Gln His His His Trp Pro Phe Gly Gly Ala Ala Cys Ser Ile Leu
100      105      110
Pro Ser Leu Ile Leu Leu Asn Met Tyr Ala Ser Ile Leu Leu Ala
115      120
Thr Ile Ser Ala Asp Arg Phe Leu Leu Val Phe Lys Pro Ile Trp Cys
125      130
Gln Asn Phe Arg Gly Ala Gly Leu Ala Trp Ile Arg Lys His Val His
135      140      145      150
Trp Gly Leu Ala Leu Leu Leu Thr Ile Pro Ser Phe Leu Tyr Arg Val
155      160      165      170
Val Arg Glu Gln Tyr Phe Pro Pro Lys Val Leu Cys Gly Val Asp Tyr
175      180      185      190
Ser His Asp Lys Arg Arg Glu Arg Ala Val Ala Ile Val Arg Leu Val
195      200      205
Leu Gly Phe Leu Trp Pro Leu Leu Thr Leu Thr Ile Cys Tyr Thr Phe
210      215      220
Ile Leu Leu Arg Thr Trp Ser Arg Arg Ala Thr Arg Ser Thr Lys Thr
225      230      235      240
Leu Lys Val Val Val Ala Val Val Ala Ser Phe Phe Ile Phe Trp Leu

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				245					250					255		
Pro	Tyr	Gln	Val	Thr	Gly	Ile	Met	Met	Ser	Phe	Leu	Glu	Pro	Ser	Ser	
			260					265					270			
Pro	Thr	Phe	Leu	Leu	Leu	Asn	Lys	Leu	Asp	Ser	Leu	Cys	Val	Ser	Phe	
		275					280					285				
Ala	Tyr	Ile	Asn	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Val	Val	Ala	Gly	
	290					295					300					
Gln	Gly	Phe	Gln	Gly	Arg	Leu	Arg	Lys	Ser	Leu	Pro	Ser	Leu	Leu	Arg	
305					310					315					320	
Asn	Val	Leu	Thr	Glu	Glu	Ser	Val	Val	Arg	Glu	Ser	Lys	Ser	Phe	Thr	
			325						330					335		
Arg	Ser	Thr	Val	Asp	Thr	Met	Ala	Gln	Lys	Thr	Gln	Ala	Val			
			340					345					350			